

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Mack, David H.
- (ii) TITLE OF INVENTION: COMPUTER-AIDED VISUALIZATION OF
EXPRESSION COMPARISON
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Joe Liebeschuetz of Townsend and Townsend and
Crew LLP
(B) STREET: Two Embarcadero Center, Eighth Floor
(C) CITY: San Francisco
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94111-3834
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 09/020,743
(B) FILING DATE: 09-FEB-1998
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Liebeschuetz, Joe
(B) REGISTRATION NUMBER: 37,505
(C) REFERENCE/DOCKET NUMBER: 018547034800US
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (650) 326-2400
(B) TELEFAX: (650) 326-2422

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2691 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

10028748-123104
PATENT "842800F"

100 Years in the Field

GGAGACAGAC	AGACAGCTGG	CAAGAGGCAG	CCTGGGGGCC	ACAGCTGCTT	CAGCAGACCT	60
CATGGCTGAG	TGAGCCTCCC	CTGGGCCCAG	CACCCACCT	CAGCATGGTC	CAAGCCCATG	120
GGGGGCGCTC	CAGAGCACAG	CCGTTGACCT	TGTCTTTGGG	GGCAGCCATG	ACCCAGCCTC	180
CGCCTGAAAA	AACGCCAGCC	AAGAAGCATG	TGCGACTGCA	GGAGAGGCGG	GGCTCCAATG	240
TGGCTCTGAT	GCTGGACGTT	CGGTCCCTGG	GGGCCGTAGA	ACCCATCTGC	TCTGTGAACA	300
CACCCCGGGA	GGTCACCTTA	CACTTTCTGC	GCACTGCTGG	ACACCCCTT	ACCCGCTGGG	360
CCCTTCAGCG	CCAGCCACCC	AGCCCCAAGC	AACTGGAAGA	AGAATTCTTG	AAGATCCCTT	420
CAAACTTTGT	CAGCCCCGAA	GACCTGGACA	TCCCTGGCCA	CGCCTCCAAG	GACCGATACA	480
AGACCATCTT	GCCAAATCCC	CAGAGCCGTG	TCTGTCTAGG	CCGGGCACAG	AGCCAGGAGG	540
ACGGAGATTA	CATCAATGCC	AACTACATCC	GAGGCTATGA	CGGGAAGGAG	AAGGTCTACA	600
TTGCCACCCA	GGGCCCCATG	CCCAACACTG	TGTCGGACTT	CTGGGAGATG	GTGTGGCAAG	660
AGGAAGTGTC	CCTCATTGTC	ATGCTCACTC	AGCTCCGAGA	GGGCAAGGAG	AAATGTGTCC	720
ACTACTGGCC	CACAGAAGAG	GAAACCTATG	GACCTTCCA	GATCCGCATC	CAGGACATGA	780
AAGAGTGCCC	AGAATACACT	GTGCGGCAGC	TCACCATCCA	GTACCAGGAA	GAGCGCCGGT	840
CAGTAAAGCA	CATCCTCTTT	TCGGCCTGGC	CAGACCATCA	GACACCAGAA	TCAGCTGGGC	900
CCCTGCTGCG	CCTAGTGGCA	GAGGTGGAGG	AGAGCCCGGA	GACAGCCGCC	CACCCCGGGC	960
CTATCGTAGT	CCACTGCAGT	GCAGGGATTG	GCCGGACGGG	CTGCTTCATC	GCCACGCGAA	1020
TTGGCTGTCA	ACAGCTGAAA	GCCCGAGGAG	AAGTGGACAT	TCTGGGTATT	GTGTGCCAAC	1080
TGCGGCTAGA	CAGAGGGGGG	ATGATCCAGA	CGGACGAGCA	GTACCAGTTC	CTGCACCACA	1140
CTTTGGCCCT	GTATGCAGGC	CAGCTGCCTG	AGGAACCCAG	CCCCTGACCC	CTGCCACCCT	1200
CCGGTGGCCC	AGGTGCCTAC	CTCCCTCAAG	CCTGGGAAGT	CACAGGAAGC	AGCAGCAGTA	1260
AGGACAAGGG	GCCGGATTCC	AGGTCTTCAA	CACTGGCCAC	TCCTCTGCTT	CCTCTGTTGG	1320
CCCCAGATGG	ACAGTAAGGG	GAACCTCCAA	TGTCTCTCTG	AACTTAAAGA	CAGGAGCTGG	1380
CATTTATGAC	AGACAAAGAA	AGAAGCCCAG	GTGTCTCTGGT	GTTCTCTGAG	AACTCTTTTG	1440
TGAGCTTCAG	TTTCCTGTTC	TATAACATGA	ACATAAGTGC	TTAGCTGCCA	TGAGGGAAAA	1500
GTAATGAGAG	AAGTTTCTAG	AAGCCACTCC	AGCCACTCCT	TCCTGGGGCT	GACAAAAGGG	1560
TGATTCCAAG	ATCATCCTTC	ACCCGAGGTC	CTGCCCAAGC	ACAGGCCAGA	TGCAAGAATG	1620
GGGAAAAGTC	TGGTCCTGAT	CTCCAAGTCT	CAACATCCTA	TCAGTGA	CTGCTCCCTGA	1680

CCACACATCG GAAGGGCTGG ATGACCCCAA TCAAAAGAAA GAACAAGGAC TCTGGTTACC 1740
 CTTGCCCTCC ACCCATGTGT CATAAGAGTA GGCTACAGAG GTGACCAGGC CTGGCAGTTG 1800
 AAATCTCTGG AAGAGGGAAC ATGTGGGGAC TACTCAGAGG CAAAGAGGAG CTGCTCCTGC 1860
 CTCCATGGTT GCTGGCCACT CCCACCAACT ACTCTTAGGG AGGCTAAGCA GTCTCTGTTT 1920
 TGCTTCCATG GCTCAAATAA TACCCTGGGT ATGCAGGACC CACTATACCT TGCATTTGCT 1980
 GGTACACCTA GAGAGCTTGG CTGTTTCCAA AAACAATCAG GGTCATAACC ATCCATGCAG 2040
 ACATGGAGGC TCGGCTGAAC CAGGACTCCT CACTGTCTAC CTGAGAGAAT GAGCACCCCT 2100
 CATCCATCTC AGCATCAACA CAATTTCCAG GGGACCTCAG GTCTACCTCA GGACTGAACG 2160
 CCACACCTCA GGATTCTCTC TCCTTGAATC TGAGACTGGC TGCCCATTCT GAGATGGGGA 2220
 TGAAGGTAAG ATGCCGCATC ACCAGGCACG CCGCCCCTGA CAGCTGCCTT GATACCAGCT 2280
 CTCTGTGGAA ACCCCCGAGG AGTTGGATCT GGAGAACAGC TGGGCCTCCT CACTCAGGAC 2340
 TTCTCTCTCG AAGAACACGC AGTGCTAAAA CTGAGGATGA TTTCCCTAAT GCTTCTGCTT 2400
 GGCCTTATGG AGGAGCTGCT CCTTCCTTAC AGCCTTGGGG ATGGACTTGC CCACACCTCC 2460
 ACCTCCCCTG AGCCCTGTGA GAGGCACGAC TGTCTATGCC AATGAGGCTC GGTGGGGGGC 2520
 TCTCAAGTGC CTGATCCTGC CCTGGGCTCA GAGCCAGCCC AGAGGGAAGC AACTGCACAG 2580
 CCCCACAGGC CCTCCCTGGC ACTGTCCCCC CAACCCCATC TCAGAGCTCA GAGGGTACAA 2640
 GCTCCAGAAC AGTAACCAAG TGGGAAAATA AAGACTTCTT GGATGACTGA C 2691

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

100242122101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Val	Gln	Ala	His	Gly	Gly	Arg	Ser	Arg	Ala	Gln	Pro	Leu	Thr	Leu	1	5	10	15
Ser	Leu	Gly	Ala	Ala	Met	Thr	Gln	Pro	Pro	Pro	Glu	Lys	Thr	Pro	Ala	20	25	30	
Lys	Lys	His	Val	Arg	Leu	Gln	Glu	Arg	Arg	Gly	Ser	Asn	Val	Ala	Leu	35	40	45	
Met	Leu	Asp	Val	Arg	Ser	Leu	Gly	Ala	Val	Glu	Pro	Ile	Cys	Ser	Val	50	55	60	
Asn	Thr	Pro	Arg	Glu	Val	Thr	Leu	His	Phe	Leu	Arg	Thr	Ala	Gly	His	65	70	75	80
Pro	Leu	Thr	Arg	Trp	Ala	Leu	Gln	Arg	Gln	Pro	Pro	Ser	Pro	Lys	Gln	85	90	95	
Leu	Glu	Glu	Glu	Phe	Leu	Lys	Ile	Pro	Ser	Asn	Phe	Val	Ser	Pro	Glu	100	105	110	
Asp	Leu	Asp	Ile	Pro	Gly	His	Ala	Ser	Lys	Asp	Arg	Tyr	Lys	Thr	Ile	115	120	125	
Leu	Pro	Asn	Pro	Gln	Ser	Arg	Val	Cys	Leu	Gly	Arg	Ala	Gln	Ser	Gln	130	135	140	
Glu	Asp	Gly	Asp	Tyr	Ile	Asn	Ala	Asn	Tyr	Ile	Arg	Gly	Tyr	Asp	Gly	145	150	155	160
Lys	Glu	Lys	Val	Tyr	Ile	Ala	Thr	Gln	Gly	Pro	Met	Pro	Asn	Thr	Val	165	170	175	
Ser	Asp	Phe	Trp	Glu	Met	Val	Trp	Gln	Glu	Glu	Val	Ser	Leu	Ile	Val	180	185	190	
Met	Leu	Thr	Gln	Leu	Arg	Glu	Gly	Lys	Glu	Lys	Cys	Val	His	Tyr	Trp	195	200	205	
Pro	Thr	Glu	Glu	Glu	Thr	Tyr	Gly	Pro	Phe	Gln	Ile	Arg	Ile	Gln	Asp	210	215	220	
Met	Lys	Glu	Cys	Pro	Glu	Tyr	Thr	Val	Arg	Gln	Leu	Thr	Ile	Gln	Tyr	225	230	235	240
Gln	Glu	Glu	Arg	Arg	Ser	Val	Lys	His	Ile	Leu	Phe	Ser	Ala	Trp	Pro	245	250	255	
Asp	His	Gln	Thr	Pro	Glu	Ser	Ala	Gly	Pro	Leu	Leu	Arg	Leu	Val	Ala	260	265	270	
Glu	Val	Glu	Glu	Ser	Pro	Glu	Thr	Ala	Ala	His	Pro	Gly	Pro	Ile	Val	275	280	285	

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Val	His	Cys	Ser	Ala	Gly	Ile	Gly	Arg	Thr	Gly	Cys	Phe	Ile	Ala	Thr
290						295					300				
Arg	Ile	Gly	Cys	Gln	Gln	Leu	Lys	Ala	Arg	Gly	Glu	Val	Asp	Ile	Leu
305					310					315					320
Gly	Ile	Val	Cys	Gln	Leu	Arg	Leu	Asp	Arg	Gly	Gly	Met	Ile	Gln	Thr
				325					330					335	
Asp	Glu	Gln	Tyr	Gln	Phe	Leu	His	His	Thr	Leu	Ala	Leu	Tyr	Ala	Gly
			340					345					350		
Gln	Leu	Pro	Glu	Glu	Pro	Ser	Pro								
		355					360								

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